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<110> Zavada, Jan
Pastorekova, Silvia
Pastorek, Jaromir

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<130> D-0021.5 PCT

<140> PCT/US99/24879

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 Met Pro Val His Pro
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<400> 7
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<400> 8
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<210> 9
 <211> 48

<212> DNA
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<223> anchor primer that anneals to the homopolymeric tail.

<220>
<221> inosine
<222> (36)..(37) (41)..(42) (46)..(47)
<223> each of the modified_bases at positions (36), (37), (41), (42), (46)
and (47) are inosine

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<400> 10
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1 5

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Gly Glu Asp Asp Pro Leu
1 5

<210> 12
<211> 21
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Tyr Gly Gly Asp Pro
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cacaccgtgt gctgggacac ccac 205

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<400> 22
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1 5

<210> 23
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<300>
<301> Locker and Buzard,
<303> DNA Sequencing and Mapping
<304> 1
<306> 3-11
<307> 1990

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<223> sequence element defined by Suzuki, J. Mol. Biol., 207: 61-84 (1989)
as motif frequently found in gene regulatory proteins.

<220>
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<222> (3)..(4)
<223> variants in sequence element defined by Suzuki, J. Mol. Biol., 207:
61-84 (1989) as motif frequently found in gene regulatory proteins.

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as a motif frequently found in gene regulatory proteins.

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<223> variants in sequence element defined by Suzuki, J. Mol. Biol., 207:
61-84 (1989) as a motif frequently found in gene regulatory proteins.

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<222> (1)..(540)

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 gaggatctac ctggagagga ggatctacct gaagttaagc ctaaatacaga agaagagggc 360
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<220>
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 <222> (1)
 <223> 2nd MN exon

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<210> 30
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<220>
 <221> exon
 <222> (1)
 <223> 3rd MN exon

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<220>
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<220>
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<210> 33
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<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 6th MN exon

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<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 9th MN exon

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<212> DNA
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<220>
<221> exon
<222> (1)
<223> 10th MN exon

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<220>
 <221> intron

<222> (1)..(193)
<223> 2nd MN intron

<400> 40
gtgagacacc caccgcgtgc acagacccaa tctgggaacc cagctctgtg gatctcccct 60
acagccgtcc ctgaacactg gtcccggggcg tcccacccgc cgcccaccgt cccaccccct 120
caccttttct acccgggttc cctaagttcc tgacctaggc gtcagacttc ctcactatac 180
tctcccaccc cag 193

<210> 41
<211> 131
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(131)
<223> 3rd MN intron

<400> 41
gtgaggggggt ctccccgccg agacttgggg atggggcggg gcgcagggaa gggaaccgtc 60
gcgcagtgcc tgcccggggg ttgggctggc cctaccgggc ggggcccggc cacttgcctc 120
tccctacgca g 131

<210> 42
<211> 89
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(89)
<223> 4th MN intron

<400> 42
gtgagcgcgg actggccgag aaggggcaaa ggagcggggc ggacgggggc cagagacgtg 60
gccctctcct accctcgtgt ccttttcag 89

<210> 43
<211> 1400
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(1400)
<223> 5th MN intron

<400> 43

gtaccagatc	ctggacaccc	cctactcccc	gctttcccat	cccatgctcc	tcccggactc	60
tatcgtggag	ccagagaccc	catcccagca	agctcactca	ggcccctggc	tgacaaactc	120
attcacgcac	tgtttgttca	tttaacaccc	actgtgaacc	aggcaccagc	ccccacaag	180
gattctgaag	ctgtagggtc	ttgcctctaa	ggagcccaca	gccagtgggg	gaggctgaca	240
tgacagacac	ataggaagga	catagtaaag	atgggtggtca	cagaggaggt	gacacttaaa	300
gccttcactg	gtagaaaaga	aaaggagggtg	ttcattgcag	aggaaacaga	atgtgcaaag	360
actcagaata	tggcctatth	aggggaatggc	tacatacacc	atgattagag	gaggcccagt	420
aaaggggaag	gatgggtgaga	tgcctgctag	gttcactcac	tcacttttat	ttattttatt	480
atthttttga	cagtctctct	gtcgcccagg	ctggagtgca	gtgggtgtgat	cttgggtcac	540
tgcaacttcc	gcctcccggg	ttcaagggat	tctcctgcct	cagcttcctg	agtagctggg	600
gttacagggtg	tgtgccacca	tgcccagcta	atthtttttt	gtatthtttag	tagacagggt	660
ttcaccatgt	tggtcagggt	ggtctcaaac	tcctggcctc	aagtgatccg	cctgactcag	720
cctaccaaa	tgctgattac	aagtgtgagc	caccgtgccc	agccacactc	actgattctt	780
taatgccagc	cacacagcac	aaagttcaga	gaaatgcctc	catcatagca	tgtcaatatg	840
ttcatactct	taggttcatg	atgttcttaa	cattagggtt	ataagcaaaa	taagaaaaaa	900
gaataataaa	taaaagaagt	ggcatgtcag	gacctcacct	gaaaagccaa	acacagaatc	960
atgaagggtga	atgcagagggt	gacaccaaca	caaagggtgt	tatatgggtt	cctgtgggga	1020
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agcctagtat	cctagtaaag	tgggctctct	ccctctctct	ccagcttgct	attgaaaacc	1140
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gattttaaga	gggagacact	gtctctaaaa	aaaaaaacaa	cagcaacaac	aaaaagcaac	1260
aaccattaca	atthttatgt	ccctcagcat	tctcagagct	gaggaatggg	agaggactat	1320
gggaaccccc	ttcatgttcc	ggccttcagc	catggccctg	gatacatgca	ctcatctgtc	1380
ttacaatgtc	attccccag					1400

<210> 44

<211> 1334

<212> DNA

<213> HUMAN

<220>

<221> intron

<222> (1)..(1334)

<223> 6th MN intron

<400> 44

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gagcttcagg	tctgaggctg	gagatgggct	ccctccagtg	caggagggat	tgaagcatga	120
gccagcgctc	atcttgataa	taaccatgaa	gctgacagac	acagttaccc	gcaaacggct	180
gcctacagat	tgaaaaccaa	gcaaaaaccg	ccggggcacg	tggctcacgc	ctgtaatccc	240
agcactttgg	gaggccaagg	cagggtggatc	acgagggtcaa	gagatcaaga	ccatcctggc	300
caacatgggtg	aaaccccatc	tctactaaaa	atacgaaaaa	atagccaggc	gtgggtggcgg	360
gtgcctgtaa	tcccagctac	tcgggagggt	gaggcaggag	aatggcatga	acccgggagg	420
cagaagttgc	agtgcagccga	gatcgtgcca	ctgcactcca	gcctgggcaa	cagagcgaga	480
ctcttgtctc	aaaaaaaaaa	aaaaaaaaaga	aaaccaagca	aaaaccaaaa	tgagacaaaa	540
aaaacaagac	caaaaaatgg	tgttttgaaa	ttgtcaagggt	caagtctgga	gagctaaact	600
ttttctgaga	actgtttatc	tttaataagc	atcaaataat	ttaactttgt	aaatactttt	660
gttggaaatc	gttctcttct	tagtcactct	tgggtcattt	taaatctcac	ttactctact	720
agacctttta	ggtttctgct	agactaggta	gaactctgcc	tttgcatthc	ttgtgtctgt	780

tttgtatagt	tatcaatatt	catatattatt	tacaagttat	tcagatcatt	ttttcttttc	840
tttttttttt	tttttttttt	ttttacatct	ttagtagaga	cagggtttca	ccatattggc	900
caggctgctc	tcaaactcct	gaccttgtga	tccaccagcc	tcggcctccc	aaagtgctgg	960
gattcatttt	ttcttttttaa	tttgctctgg	gcttaaactt	gtggcccagc	actttatgat	1020
ggtacacaga	gttaagagtg	tagactcaga	cggctcttct	tctttccttc	tcttccttcc	1080
tcccttccct	cccaccttcc	cttctctcct	tcctttcttt	cttctctctc	tgcttctca	1140
ggcctcttcc	agttgctcca	aagccctgta	cttttttttg	agttaacgtc	ttatgggaag	1200
ggcctgcact	tagtgaagaa	gtggtctcag	agttgagtta	ccttggcttc	tgggaggtga	1260
aactgtatcc	ctataccctg	aagctttaag	ggggtgcaat	gtagatgaga	ccccaacata	1320
gacctcttc	acag					1334

<210> 45
 <211> 512
 <212> DNA
 <213> HUMAN

<220>
 <221> intron
 <222> (1)..(512)
 <223> 7th MN intron

<400> 45						
gtgggcctgg	ggtgtgtgtg	gacacagtgg	gtgcggggga	aagaggatgt	aagatgagat	60
gagaaacagg	agaagaaaga	aatcaaggct	gggctctgtg	gcttacgcct	ataatcccac	120
cacgttgga	ggctgaggtg	ggagaatgg	ttgagcccag	gagttcaaga	caaggcgggg	180
caacatagtg	tgaccccatc	tctaccaaaa	aaaccccaac	aaaaccaaaa	atagccgggc	240
atggtggtat	gcggcctagt	cccagctact	caaggaggct	gaggtgggaa	gatcgcttga	300
ttccaggagt	ttgagactgc	agtgagctat	gatcccacca	ctgcctacca	tctttaggat	360
acatttat	atattataaaa	gaaatcaaga	ggctggatgg	ggaatacagg	agctggaggg	420
tggagccctg	aggtgctgg	tgtgagctgg	cctgggaccc	ttgtttcctg	tcatgccatg	480
aaccaccca	cactgtccac	tgacctccct	ag			512

<210> 46
 <211> 114
 <212> DNA
 <213> HUMAN

<220>
 <221> intron
 <222> (1)..(114)
 <223> 8th MN intron

<400> 46						
gtacagcttt	gtctgggtttc	ccccagcca	gtagtccctt	atcctcccat	gtgtgtgcc	60
gtgtctgtca	ttgggtgggtca	cagcccgcct	ctcacatctc	ctttttctct	ccag	114

<210> 47
 <211> 617

<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(617)
<223> 9th MN intron

<400> 47
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agggctgctc aggaccgcct ctgctccctc tccttttctg cagaacagac cccaacccca 120
atattagaga ggcagatcat ggtggggatt cccccattgt ccccagaggc taattgatta 180
gaatgaagct tgagaaatct cccagcatcc ctctcgcaaa agaatcccc cccctttttt 240
taaagatagg gtctcactct gtttgcccca ggctgggggtg ttgtggcacg atcatagctc 300
actgcagcct cgaactccta ggctcaggca atcctttcac cttagcttct caaagcactg 360
ggactgtagg catgagccac tgtgcctggc cccaaacggc ccttttactt ggcttttagg 420
aagcaaaaac ggtgcttata ttacccttcc tcgtgtatcc accctcatcc cttggctggc 480
ctcttctgga gactgaggca ctatggggct gcctgagaac tcggggcagg ggtggtggag 540
tgcactgagg caggtgttga ggaactctgc agaccctct tccttcccaa agcagccctc 600
tctgctctcc atcgag 617

<210> 48
<211> 130
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(130)
<223> 10th MN intron

<400> 48
gtattacact gaccctttct tcaggcacia gcttccccca cccttgtgga gtcacttcat 60
gcaaagcgca tgcaaataag ctgctcctgg gccagttttc tgattagcct ttcctgttgt 120
gtacacacag 130

<210> 49
<211> 1401
<212> DNA
<213> HUMAN

<400> 49
caaactttca cttttgttgc ccaggctgga gtgcaatggc gcgatctcgg ctcactgcaa 60
cctccacctc ccgggttcaa gtgattctcc tgcctcagcc tctagccaag tagctgcgat 120
tacaggcatg cgccaccacg cccggctaata ttttgtattt ttagtagaga cgggggtttcg 180
ccatgttggt caggctggtc tcgaactcct gatctcaggt gatccaacca ccctggcctc 240
ccaaagtgct gggattatag gcgtgagcca cagcgctgg cctgaagcag ccactcactt 300
ttacagaccc taagacaatg attgcaagct ggtaggattg ctgtttggcc caccagctg 360
cggtgttgag tttgggtgag gtctcctgtg ctttgcacct ggcccgtta aggcatttgt 420

tacccgtaat	gctcctgtaa	ggcatctgcg	tttgtgacat	cgtttttggtc	gccaggaagg	480
gattggggct	ctaagcttga	gcggttcac	cttttcattt	atacagggga	tgaccagagt	540
cattggcgct	atggagggtga	gacacccacc	cgctgcacag	acccaatctg	ggaacccagc	600
tctgtggatc	tcccctacag	ccgtccctga	acactgggtcc	cgggcggtccc	acccgcccgc	660
caccgtccca	ccccctcacc	ttttctaccc	gggttcccta	agttcctgac	ctaggcggtca	720
gacttcctca	ctataactctc	ccaccccagg	cgacccgccc	tggccccggg	tgtccccagc	780
ctgcgcgggc	cgcttccagt	ccccgggtgga	tatccgcccc	cagctcgccg	ccttctgccc	840
ggccctgcmc	cccctggaac	tcctgggctt	ccagctcccc	ccgctcccag	aactgcmcct	900
gcgcaacaat	ggccacagtg	gtgagggggg	ctccccgccc	agacttgggg	atggggcggg	960
gcgcagggaa	gggaaccgtc	gcgcagtgcc	tgccccgggg	ttgggctggc	cctaccgggc	1020
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atggctctgg	gtcccggggc	ggagtaccgg	gctctgcagc	tgcactctga	ctgggggggt	1140
gcaggctcgtc	cgggctcgga	gcacactgtg	gaaggccacc	gtttccctgc	cgagggtgagc	1200
gcggactggc	cgagaagggg	caaaggagcg	gggcggacgg	gggcccagaga	cgtggcccctc	1260
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ttgacgaggc	cttggggcmc	ccgggaggcc	tggccgtgtt	ggccgccttt	ctggagggtac	1380
cagatcctgg	acacccccta	c				1401

<210> 50
 <211> 59
 <212> PRT
 <213> HUMAN

<400> 50
 Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu
 1 5 10 15
 Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro
 20 25 30
 Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro
 35 40 45
 Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu
 50 55

<210> 51
 <211> 257
 <212> PRT
 <213> HUMAN

<400> 51
 Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp Pro
 1 5 10 15
 Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp Ile
 20 25 30

Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu Leu
 35 40 45
 Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn Asn
 50 55 60
 Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala Leu
 65 70 75 80
 Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp Gly
 85 90 95
 Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg Phe
 100 105 110
 Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg Val
 115 120 125
 Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala Phe
 130 135 140
 Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu Ser
 145 150 155 160
 Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro Gly
 165 170 175
 Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe Gln
 180 185 190
 Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile Trp
 195 200 205
 Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His Thr
 210 215 220
 Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn
 225 230 235 240
 Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe
 245 250 255

Pro

<210> 52
 <211> 20
 <212> PRT
 <213> HUMAN

<400> 52

Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala
1 5 10 15

Phe Leu Val Gln
20

<210> 53

<211> 25

<212> PRT

<213> HUMAN

<400> 53

Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg
1 5 10 15

Pro Ala Glu Val Ala Glu Thr Gly Ala
20 25

<210> 54

<211> 59

<212> PRT

<213> HUMAN

<400> 54

Ser Ala Ser Glu Glu Pro Ser Pro Ser Glu Val Pro Phe Pro Ser Glu
1 5 10 15

Glu Pro Ser Pro Ser Glu Glu Pro Phe Pro Ser Val Arg Pro Phe Pro
20 25 30

Ser Val Val Leu Phe Pro Ser Glu Glu Pro Phe Pro Ser Lys Glu Pro
35 40 45

Ser Pro Ser Glu Glu Pro Ser Ala Ser Glu Glu
50 55

<210> 55

<211> 470

<212> RNA

<213> HUMAN

<400> 55

cauggcccccg auaaccuucu gccugugcac acaccugccc cucacuccac ccccauccua 60
gcuuugguau gggggagagg gcacagggcc agacaaaccu gugagacuuu ggcuccaucu 120
cugcaaaagg ggcgucugug agucagccug cccccucca ggcugucc uccccaccc 180
agcucucguu uccaaugcac guacagcccc uacacaccgu gugcugggac accccacagu 240
cagccgcaug gcuccccugu gccccagccc cuggcucccu cuguugaucc cggccccugc 300

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uccagggccuc acugugcaac ugcugcuguc acugcugcuu cuggugccug uccaucucca 360
gagguugccc cggaugcagg aggauucccc cuugggagga ggcucuucug gggaagauga 420
cccacugggc gaggaggauca ugcccaguga agaggauuca cccagagagg          470
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```
<210> 56
<211> 292
<212> DNA
<213> HUMAN
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<400> 56
gttttttttga gacggagtct tgcattctgtc atgcccaggc tggagttagca gtggtgccat 60
ctcggctcac tgcaagctcc acctcccgag ttcacgccat tttcctgcct cagcctcccg 120
agtagctggg actacaggcg cccgccacca tgcccggcta attttttgta tttttggtag 180
agacgggggtt tcaccgtggt agccagaatg gtctcgatct cctgacttcg tgatccaccc 240
gcctcggcct cccaaagtgc tgggattaca ggtgtgagcc accgcacctg gc          292
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```
<210> 57
<211> 262
<212> DNA
<213> HUMAN
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<400> 57
tttctttttt gagacagggt cttgctctgt caccaggcc agagtgcaat ggtacagtct 60
cagctcactg cagcctcaac cgcctcggct caaaccatca tcccatattca gcctcctgag 120
tagctgggac tacaggcaca tgccattaca cctggctaata ttttttgtag ttctagtaga 180
gacagggttt ggccatgttg cccgggctgg tctcgaactc ctggactcaa gcaatccacc 240
cacctcagcc tcccaaaatg ag          262
```

```
<210> 58
<211> 2501
<212> DNA
<213> HUMAN
```

```
<220>
<221> misc_feature
<222> (1)..(2501)
<223> region 5' to transcription initiation site as determined by RNase
protection assay (nucleotide 3507 of Figures 2A-2F and of SEQ ID NO: 5),
corresponding to region of SEQ ID NO: 5 and Figures 2A-2F from nucleotide
(7) to nucleotide (2507), in which region some regulatory elements are
probably situated.
```

```
<220>
<221> unsure what base is at position 1968
<222> (1968)
<223> unsure of base at position 1968, which is the same unknown base as
that at position 1974 of SEQ ID NO. 5, i.e., the full-length MN genomic
sequence, and of that unknown at position 1968 of SEQ ID NO: 90, and
```

unknown at position 647 of SEQ ID NO: 110. That unknown base is in the 5' region flanking the transcription initiation site (3507) as determined by RNase protection assay.

<400> 58

tggtgactcg	tgaccttacc	cccaaccctg	tgctctctga	aacatgagct	gtgtccactc	60
agggttaa	ggattaaggg	cggtgcaaga	tgtgctttgt	taaacagatg	cttgaaggca	120
gcatgctcgt	taagagtc	caccaatccc	taatctcaag	taatcaggga	cacaaacact	180
gcggaaggcc	gcagggtcct	ctgcctagga	aaaccagaga	cctttgttca	cttgtttatc	240
tgaccttccc	tccactattg	tccatgaccc	tgccaaatcc	ccctctgtga	gaaacaccca	300
agaattatca	ataaaaaaat	aaatttataa	aaaaaatata	aaaaaaaaaa	aaaaaaaaaa	360
aaaagactta	cgaatagtta	ttgataaatg	aatagctatt	ggtaaagcca	agtaa	420
catattcaaa	accagacggc	catcatcaca	gctcaagtct	acctgatttg	atctctttat	480
cattgtcatt	ctttggattc	actagattag	tcatcatcct	caaaattctc	ccccaagttc	540
taattacg	ccaaacattt	aggggttaca	tgaagcttga	acctactacc	ttctttgctt	600
ttgagccatg	agttgtagga	atgatgagtt	tacaccttac	atgctgggga	ttaattttaa	660
ctttacctct	aagtcagttg	ggtagccttt	ggcttatttt	tgtagcta	tttgtagtta	720
atggatgcac	tgtgaatctt	gctatgatag	ttttcctcca	cactttgcca	ctaggggtag	780
gtaggtactc	agttttcagt	aattgcttac	ctaagaccct	aagccctatt	tctcttgtag	840
tggcctttat	ctgtaatatg	ggcataattta	atacaatata	atttttggag	tttttttggt	900
tgtttg	tttg	tgagacggag	tcttgcatct	gtcatgccca	ggctggagta	960
gcagtgg	catctcggct	cactgcaagc	tccacctccc	gagttcacgc	cattttcctg	1020
cctcagcctc	ccgagtagct	gggactacag	gcgcccgcga	ccatgcccgg	ctaatttttt	1080
gtatttttgg	tagagacggg	gtttcacctg	gttagccaga	atgggtctcg	tctcctgact	1140
tcgtgatcca	cccgctcgg	cctcccaaag	ttctgggatt	acaggtgtga	gccaccgcac	1200
ctggccaatt	ttttgagtct	tttaaagtaa	aaatatgtct	tgtaagctgg	taactatggt	1260
acatttcctt	ttattaatgt	ggtgctgacg	gtcatatagg	ttcttttgag	tttggcatgc	1320
atatgctact	ttttgcagtc	ctttcattac	atttttctct	cttcatttga	agagcatggt	1380
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ttgttattgg	atatcatcat	tggcccacgc	tttctgacct	tggaaacaat	taagggttca	1860
taatctcaat	tctgtcagaa	ttgggtacaag	aaatagctgc	tatgtttctt	gacattccac	1920
ttggtaggaa	ataagaatgt	gaaactcttc	agttgggtgtg	tgtccctngt	ttttttgcaa	1980
tttccttctt	actgtgttaa	aaaaaagtat	gatcttgctc	tgagaggtga	ggcattctta	2040
atcatgatct	ttaaagatca	ataatataat	cctttcaagg	attatgtctt	tattataata	2100
aagataa	gtctttaaca	gaatcaataa	tataatccct	taaaggatta	tatctttgct	2160
gggcgcagtg	gctcacacct	gtaatcccag	cactttgggt	ggccaagggtg	gaaggatcaa	2220
atttgcctac	ttctatatta	tcttctaaag	cagaattcat	ctctcttccc	tcaatatgat	2280
gatattgaca	gggtttgccc	tactcacta	gattgtgagc	tcctgctcag	ggcaggtagc	2340
gttttttggt	tttg	tttttctttt	ttgagacagg	gtcttgctct	gtcaccag	2400
ccagagtgca	atgggtacagt	ctcagctcac	tgcagcctca	accgcctcgg	ctcaaaccat	2460
catcccattt	cagcctcctg	agtagctggg	actacaggca	c		2501

<210> 59

<211> 292

<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)

<400> 59
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gtagctggga ctacaggcgc ccgccaccat gcccggttaa ttttttgtat ttttggtaga 180
gacgggggtt caccgtgtta gccagaatgg tctcgatctc ctgacttcgt gatccacccg 240
cctcggcctc ccaaagttct gggattacag gtgtgagcca ccgcacctgg cc 292

<210> 60
<211> 262
<212> DNA
<213> HUMAN

<400> 60
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agctcactgc agcctcaacc gcctcggctc aaaccatcat cccatttcag cctcctgagt 120
agctgggact acaggcacat gccattacac ctggctaatt tttttgtatt tctagtagag 180
acagggtttg gccatgttgc ccgggctggg ctcgaaactcc tggactcaag caatccaccc 240
acctcagcct cccaaaatga gg 262

<210> 61
<211> 294
<212> DNA
<213> HUMAN

<400> 61
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cggctcactg caacctccac ctcccgggtt caagtgattc tcctgcctca gcctctagcc 120
aagtagctgc gattacaggc atgcgccacc acgcccggct aatttttgta ttttttagtag 180
agacgggggtt tcgccatgtt ggtcaggctg gtctcgaact cctgatctca ggtgatccaa 240
ccaccctggc ctcccaaagt gctgggatta taggcgtgag ccacagcgcc tggc 294

<210> 62
<211> 276
<212> DNA
<213> HUMAN

<400> 62
tgacagtctc tctgtcgccc aggctggagt gcagtgggtg gatcttgggt cactgcaact 60
tccgcctccc gggttcaagg gattctcctg cctcagcttc ctgagtagct ggggttacag 120
gtgtgtgcca ccatgcccag ctaatttttt tttgtatttt tagtagacag ggtttcacca 180
tgttgggtcag gctgggtctc aactcctggc ctcaagtgat ccgcctgact cagcctacca 240

aagtgctgat tacaagtgtg agccaccgtg cccagc

276

<210> 63
<211> 289
<212> DNA
<213> HUMAN

<400> 63
cgccggggcac ggtgggtcac gcctgtaatc ccagcacttt gggaggccaa ggcagggtgga 60
tcacgagggtc aagagatcaa gaccatcctg gccaacatgg tgaaacccca tctctactaa 120
aaatacga aaatagccag gcgtgggtggc ggggtgcctgt aatcccagct actcgggagg 180
ctgaggcagg agaatggcat gaacccggga ggcagaagtt gcagtgagcc gagatcgtgc 240
cactgcactc cagcctgggc aacagagcga gactcttgtc tcaaaaaaa 289

<210> 64
<211> 298
<212> DNA
<213> HUMAN

<400> 64
aggctgggct ctgtggctta cgcctataat cccaccacgt tgggaggctg aggtgggaga 60
atggtttgag cccaggagtt caagacaagg cggggcaaca tagtgtgacc ccatctctac 120
caaaaaaacc ccaacaaaac caaaaatagc cgggcatggg ggtatgcggc ctagtcccag 180
ctactcaagg aggctgaggt gggaagatcg cttgattcca ggagtttgag actgcagtga 240
gctatgatcc caccactgcc taccatcttt aggatacatt tattttattta taaaagaa 298

<210> 65
<211> 105
<212> DNA
<213> HUMAN

<400> 65
ttttttacat ctttagtaga gacagggttt caccatattg gccaggctgc tctcaaactc 60
ctgaccttgt gatccaccag cctcggcctc ccaaagtgtc gggat 105

<210> 66
<211> 83
<212> DNA
<213> HUMAN

<400> 66
cctcgaactc ctaggctcag gcaatccttt caccttagct tctcaaagca ctgggactgt 60
aggcatgagc cactgtgcct ggc 83

<210> 67
<211> 11

<212> DNA
<213> HUMAN

<400> 67
agaaggtaag t 11

<210> 68
<211> 11
<212> DNA
<213> HUMAN

<400> 68
tggagggtgag a 11

<210> 69
<211> 11
<212> DNA
<213> HUMAN

<400> 69
cagtcgtgag g 11

<210> 70
<211> 11
<212> DNA
<213> HUMAN

<400> 70
ccgagggtgag c 11

<210> 71
<211> 11
<212> DNA
<213> HUMAN

<400> 71
tggaggtacc a 11

<210> 72
<211> 11
<212> DNA
<213> HUMAN

<400> 72
ggaaggtcag t 11

<210> 73
<211> 11
<212> DNA
<213> HUMAN

<400> 73
agcaggtggg c 11

<210> 74
<211> 11
<212> DNA
<213> HUMAN

<400> 74
gccaggtaca g 11

<210> 75
<211> 11
<212> DNA
<213> HUMAN

<400> 75
tgctgggtgag t 11

<210> 76
<211> 11
<212> DNA
<213> HUMAN

<400> 76
cacaggtatt a 11

<210> 77
<211> 11
<212> DNA
<213> HUMAN

<400> 77
atacagggga t 11

<210> 78
<211> 11
<212> DNA
<213> HUMAN

<400> 78

ccccaggcga c 11

<210> 79
<211> 11
<212> DNA
<213> HUMAN

<400> 79
acgcagtgca a 11

<210> 80
<211> 11
<212> DNA
<213> HUMAN

<400> 80
tttcagatcc a 11

<210> 81
<211> 11
<212> DNA
<213> HUMAN

<400> 81
ccccaggagg g 11

<210> 82
<211> 11
<212> DNA
<213> HUMAN

<400> 82
tcacaggctc a 11

<210> 83
<211> 11
<212> DNA
<213> HUMAN

<400> 83
ccctagctcc a 11

<210> 84
<211> 11
<212> DNA

<213> HUMAN

<400> 84

ctccagtcca g

11

<210> 85

<211> 12

<212> DNA

<213> HUMAN

<400> 85

tcgcaggtga ca

12

<210> 86

<211> 11

<212> DNA

<213> HUMAN

<400> 86

acacagaagg g

11

<210> 87

<211> 377

<212> PRT

<213> HUMAN

<400> 87

Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly Gly Ser
1 5 10 15

Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu Glu
20 25 30

Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly
35 40 45

Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro Lys
50 55 60

Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp Leu Pro Thr Val Glu
65 70 75 80

Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
85 90 95

Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
100 105 110

Pro	Arg	Val	Ser	Pro	Ala	Cys	Ala	Gly	Arg	Phe	Gln	Ser	Pro	Val	Asp
		115					120					125			
Ile	Arg	Pro	Gln	Leu	Ala	Ala	Phe	Cys	Pro	Ala	Leu	Arg	Pro	Leu	Glu
	130					135					140				
Leu	Leu	Gly	Phe	Gln	Leu	Pro	Pro	Leu	Pro	Glu	Leu	Arg	Leu	Arg	Asn
145					150					155					160
Asn	Gly	His	Ser	Val	Gln	Leu	Thr	Leu	Pro	Pro	Gly	Leu	Glu	Met	Ala
				165					170					175	
Leu	Gly	Pro	Gly	Arg	Glu	Tyr	Arg	Ala	Leu	Gln	Leu	His	Leu	His	Trp
			180					185					190		
Gly	Ala	Ala	Gly	Arg	Pro	Gly	Ser	Glu	His	Thr	Val	Glu	Gly	His	Arg
		195					200					205			
Phe	Pro	Ala	Glu	Ile	His	Val	Val	His	Leu	Ser	Thr	Ala	Phe	Ala	Arg
	210					215					220				
Val	Asp	Glu	Ala	Leu	Gly	Arg	Pro	Gly	Gly	Leu	Ala	Val	Leu	Ala	Ala
225					230					235					240
Phe	Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	Tyr	Glu	Gln	Leu	Leu
				245					250					255	
Ser	Arg	Leu	Glu	Glu	Ile	Ala	Glu	Glu	Gly	Ser	Glu	Thr	Gln	Val	Pro
			260					265					270		
Gly	Leu	Asp	Ile	Ser	Ala	Leu	Leu	Pro	Ser	Asp	Phe	Ser	Arg	Tyr	Phe
		275					280					285			
Gln	Tyr	Glu	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Ala	Gln	Gly	Val	Ile
	290					295					300				
Trp	Thr	Val	Phe	Asn	Gln	Thr	Val	Met	Leu	Ser	Ala	Lys	Gln	Leu	His
305					310					315					320
Thr	Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	Ser	Arg	Leu	Gln	Leu
				325					330					335	
Asn	Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	Val	Ile	Glu	Ala	Ser
			340					345					350		
Phe	Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro	Arg	Ala	Ala	Glu	Pro	Val	Gln
		355					360					365			
Leu	Asn	Ser	Cys	Leu	Ala	Ala	Gly	Asp							
	370					375									

<210> 88
<211> 34
<212> DNA
<213> HUMAN

<400> 88
tagacagatc tacgatggct cccctgtgcc ccag 34

<210> 89
<211> 34
<212> DNA
<213> HUMAN

<400> 89
attcctctag acagttaccg gctccccctc agat 34

<210> 90
<211> 3532
<212> DNA
<213> HUMAN

<220>
<221> misc_feature which includes the MN gene promoter
<222> (1)..(3532)
<223> region including the transcription initiation site (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) as determined by RNase protection assay, which region is inclusive of the MN gene promoter, and corresponds to nucleotide 7 to nucleotide 3538 of SEQ ID NO: 5 and of Figures 2A-2F.

<220>
<221> unsure what base is at position 1968
<222> (1968)
<223> unsure of the base at position 1968, which is the same unknown base at position 1974 of SEQ ID NO: 5 (the full-length MN genomic sequence), position 1968 of SEQ ID NO: 58 and position 647 of SEQ ID NO: 110. That unknown base is in the region that includes the transcription initiation site (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) as determined by RNase protection assay, which region is inclusive of the MN gene promoter.

<400> 90
tggtgactcg tgaccttacc cccaaccctg tgctctctga aacatgagct gtgtccactc 60
agggttaaataa ggattaaggg cggtgcaaga tgtgctttgt taaacagatg cttgaaggca 120
gcatgctcgt taagagtcac caccaatccc taatctcaag taatcaggga cacaaacact 180
gcggaaggcc gcagggtcct ctgcctagga aaaccagaga cctttgttca cttgtttatc 240
tgaccttccc tccactattg tccatgaccc tgccaaatcc ccctctgtga gaaacaccca 300
agaattatca ataaaaaaat aaatttataa aaaaaatata aaaaaaaaaa aaaaaaaaaa 360
aaaagactta cgaatagtta ttgataaatg aatagctatt ggtaaagcca agtaaatgat 420
catattcaaa accagacggc catcatcaca gctcaagtct acctgatttg atctctttat 480

cattgtcatt	ctttggattc	actagattag	tcatcatcct	caaaattctc	ccccaagttc	540
taattacgtt	ccaaacattt	aggggttaca	tgaagcttga	acctactacc	ttcttttgctt	600
ttgagccatg	agttgtagga	atgatgagtt	tacaccttac	atgctgggga	ttaatTTaaa	660
ctttacctct	aagtcagttg	ggtagccttt	ggcttatttt	tgtagctaata	tttgtagtta	720
atggatgcac	tgtgaatctt	gctatgatag	ttttcctcca	cactttgcca	ctaggggtag	780
gtaggtactc	agttttcagt	aattgcttac	ctaagaccct	aagccctatt	tctcttgtag	840
tggcctttat	ctgtaatatg	ggcatattta	atacaatata	atTTTTtgag	tttttttggt	900
tgtttgtttg	tttgtttttt	tgagacggag	tcttgcatct	gtcatgcccc	ggctggagta	960
gcagtgggtgc	catctcggct	cactgcaagc	tccacctccc	gagttcacgc	cattttcctg	1020
cctcagcctc	ccgagtagct	gggactacag	gcgccccgca	ccatgcccgg	ctaatttttt	1080
gtatTTTTtg	tagagacggg	gtttcacctg	gttagccaga	atggctctga	tctcctgact	1140
tcgtgatcca	cccgctcgg	cctcccaaag	ttctgggatt	acaggtgtga	gccaccgcac	1200
ctggccaatt	ttttgagtct	tttaaagtaa	aaatatgtct	tgtaagctgg	taactatggg	1260
acatttcctt	ttattaatgt	ggtgctgacg	gtcataatagg	ttcttttgag	tttggcatgc	1320
atatgctact	ttttgcagtc	ctttcattac	atTTTTtctct	cttcatttga	agagcatggt	1380
atatctttta	gcttcacttg	gcttaaaaagg	ttctctcatt	agcctaacac	agtgtcattg	1440
ttggtaccac	ttggatcata	agtggaaaaa	cagtcaagaa	attgcacagt	aatacttggt	1500
tgtaagaggg	atgattcagg	tgaatctgac	actaagaaac	tccctacct	gaggtctgag	1560
attcctctga	cattgctgta	tataggcttt	tcctttgaca	gcctgtgact	gcggactatt	1620
tttcttaagc	aagatatgct	aaagttttgt	gagccttttt	ccagagagag	gtctcatatc	1680
tgcatacaagt	gagaacatat	aatgtctgca	tgtttccata	tttcaggaat	gtttgcttgt	1740
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ttgttattgg	atatcatcat	tggcccacgc	tttctgacct	tggaaacaat	taaggggtca	1860
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tttccttctt	actgtgttaa	aaaaaagtat	gatcttgctc	tgagaggtga	ggcattctta	2040
atcatgatct	ttaaagatca	ataatataat	cctttcaagg	attatgtctt	tattataata	2100
aagataattt	gtctttaaca	gaatcaataa	tataatccct	taaaggatta	tatctttgct	2160
gggcgcagtg	gctcacacct	gtaatcccag	cactttgggt	ggccaagggtg	gaaggatcaa	2220
at ttgcctac	ttctatatta	tcttctaaag	cagaattcat	ctctcttccc	tcaatatgat	2280
gatattgaca	gggtttgccc	tcactcacta	gattgtgagc	tcctgctcag	ggcaggtagc	2340
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ccagagtgca	atgggtacagt	ctcagctcac	tgcagcctca	accgcctcgg	ctcaaaccat	2460
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aaaggtttgg	agaaaaaaat	aatagtttaa	tttggctaga	gtatgaggga	gagtagtagg	2820
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caatgtgcat	atcgtggcag	gcagtgggga	gccaatgaag	gcttttgagc	aggagagtaa	2940
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tttcattcaa	gctcaagttt	gtctcccaca	taccattac	ttaaactcacc	ctcgggctcc	3060
cctagcagcc	tgcctacct	ctttacctgc	ttcttggtgg	agtcagggat	gtatacatga	3120
gctgctttcc	ctctcagcca	gaggacatgg	ggggccccag	ctcccctgcc	tttccccttc	3180
tgtgcctgga	gctgggaagc	aggccagggg	tagctgaggc	tggctggcaa	gcagctgggt	3240
ggtgccaggg	agagcctgca	tagtgccagg	tgggtgcctg	ggttccaagc	tagtccatgg	3300
ccccgataac	cttctgcctg	tgcacacacc	tgcccctcac	tccacccccca	tcctagcttt	3360
ggtatggggg	agagggcaca	gggccagaca	aacctgtgag	actttggctc	catctctgca	3420
aaagggcgct	ctgtgagtca	gcctgctccc	ctccaggctt	gctcctcccc	caccagctc	3480
tcgtttccaa	tgcacgtaca	gcccgtacac	accgtgtgct	gggacacccc	ac	3532

<210> 91
<211> 204
<212> DNA
<213> HUMAN

<400> 91
cctgcccctc actccacccc catcctagct ttggtatggg ggagagggca cagggccaga 60
caaacctgtg agactttggc tccatctctg caaaagggcg ctctgtgagt cagcctgctc 120
ccctccaggc ttgctcctcc cccacccagc tctcgtttcc aatgcacgta cagcccgtac 180
acaccgtgtg ctgggacacc ccac 204

<210> 92
<211> 132
<212> DNA
<213> HUMAN

<400> 92
ggatcctggt gactcgtgac cttaccccca accctgtgct ctctgaaaca tgagctgtgt 60
ccactcaggg ttaaatggat taagggcggt gcaagatgtg ctttggttaa cagatgcttg 120
aaggcagcat gc 132

<210> 93
<211> 275
<212> DNA
<213> HUMAN

<400> 93
gcatagtgcc aggtggtgcc ttgggttcca agctagtcca tggccccgat aaccttctgc 60
ctgtgcacac acctgcccct cactccaccc ccatactagc ttggtatgg gggagagggc 120
acagggccag acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag 180
tcagcctgct cccctccagg cttgctcctc cccacccag ctctcgtttc caatgcacgt 240
acagcccgtg cacaccgtgt gctgggacac cccac 275

<210> 94
<211> 89
<212> DNA
<213> HUMAN

<400> 94
ctgctcccct ccaggcttgc tectccccca cccagctctc gtttccaatg cacgtacagc 60
ccgtacacac cgtgtgctgg gacacccca 89

<210> 95
<211> 61
<212> DNA
<213> HUMAN

<400> 95
caccagctc tcgtttccaa tgcacgtaca gcccgtagac accgtgtgct gggacacccc 60
a 61

<210> 96
<211> 116
<212> DNA
<213> HUMAN

<400> 96
acctgccct cactccaccc ccatactagc ttgggtatgg gggagagggc acagggccag 60
acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag tcagcc 116

<210> 97
<211> 36
<212> PRT
<213> HUMAN

<400> 97
Gly Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp
1 5 10 15
Pro Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu
20 25 30
Glu Asp Leu Pro
35

<210> 98
<211> 6
<212> PRT
<213> HUMAN

<400> 98
Gly Glu Glu Asp Leu Pro
1 5

<210> 99
<211> 4
<212> PRT
<213> HUMAN

<400> 99
Glu Glu Asp Leu
1

<210> 100
<211> 5
<212> PRT
<213> HUMAN

<400> 100
Glu Glu Asp Leu Pro
1 5

<210> 101
<211> 6
<212> PRT
<213> HUMAN

<400> 101
Glu Asp Leu Pro Ser Glu
1 5

<210> 102
<211> 7
<212> PRT
<213> HUMAN

<400> 102
Glu Glu Asp Leu Pro Ser Glu
1 5

<210> 103
<211> 6
<212> PRT
<213> HUMAN

<400> 103
Asp Leu Pro Gly Glu Glu
1 5

<210> 104
<211> 22
<212> PRT
<213> HUMAN

<400> 104
Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro
1 5 10 15

Ser Glu Glu Asp Ser Pro
20

<210> 105
<211> 25
<212> PRT
<213> HUMAN

<400> 105
Gly Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp
1 5 10 15
Pro Pro Gly Glu Glu Asp Leu Pro Gly
20 25

<210> 106
<211> 24
<212> PRT
<213> HUMAN

<400> 106
Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
1 5 10 15
Gly Glu Glu Asp Leu Pro Glu Val
20

<210> 107
<211> 7
<212> PRT
<213> HUMAN

<400> 107
Gly Glu Thr Arg Ala Pro Leu
1 5

<210> 108
<211> 7
<212> PRT
<213> HUMAN

<400> 108
Gly Glu Thr Arg Glu Pro Leu
1 5

<210> 109
<211> 7
<212> PRT
<213> HUMAN

<400> 109
 Gly Gln Thr Arg Ser Pro Leu
 1 5

<210> 110
 <211> 1247
 <212> DNA
 <213> HUMAN

<220>
 <221> misc_feature
 <222> (1)..(1247)
 <223> region 5' to the transcription initiation site as determined by RNase protection assay (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) in which an activating element is localized, which region corresponds to nucleotide 1328 to nucleotide 2574 of SEQ ID NO: 5 and of Figures 2A-2F.

<220>
 <221> unsure what base is at position 647
 <222> (647)
 <223> unsure of the base at position 647, which is the same unknown base as that at position 1974 of SEQ ID NO: 5, and as that at position 1968 of SEQ ID NOS: 58 and 90. That unknown base at position 647 is in a region in which an activating element is localized and is 5' to the transcription initiation site.

<400> 110
 tatgctactt tttgcagtcc tttcattaca tttttctctc ttcatttgaa gagcatgtta 60
 tatcttttag cttcacttgg cttaaaagggt tctctcatta gcctaacaca gtgtcattgt 120
 tggtagcact tggatcataa gtggaaaaaac agtcaagaaa ttgcacagta atacttggtt 180
 gtaagaggga tgattcaggt gaatctgaca ctaagaaact cccctacctg aggtctgaga 240
 ttcctctgac attgctgtat ataggctttt cctttgacag cctgtgactg cggactattt 300
 ttcttaagca agatatgcta aagttttgtg agcctttttc cagagagagg tctcatatct 360
 gcatcaagtg agaacatata atgtctgcat gtttccatat ttcaggaatg tttgcttgtg 420
 ttttatgctt ttatatagac agggaaactt gttcctcagt gacccaaaag aggtgggaat 480
 tggtattgga tatcatcatt ggcccacgct ttctgacctt ggaaacaatt aagggttcat 540
 aatctcaatt ctgtcagaat tggtagaaga aatagctgct atgtttcttg acattccact 600
 tggtaggaaa taagaatgtg aaactcttca gttggtgtgt gtccctngtt tttttgcaat 660
 ttccttctta ctgtgttaaa aaaaagtatg atcttgctct gagagggtgag gcattcttaa 720
 tcatgatctt taaagatcaa taatataatc ctttcaagga ttatgtcttt attataataa 780
 agataatttg tctttaacag aatcaataat ataatccctt aaaggattat atctttgctg 840
 ggcgcagtgg ctcacacctg taatcccagc actttgggtg gccaaagggtg aaggatcaaa 900
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